

Fig.1

C2GnT3

1	M K I F K C Y F K H T I Q Q K V F I L E L T L W L L S S L L K L L N V R R L F P Q	40
1	ATGAAAGATATTCAATGTTTAAACATACCCCTACAGAGAAAGTTTACCCATTGGCTCTCTTGTAAAGCTTCTAAATGTGAGGGACTCTTCCCAA	120
41	K D I Y L V E Y S L S T S P F V R N R Y T H V K D E V R Y E V N C S G I Y E Q E	80
121	AAAGACATTACTGGTGTGAGTACTCCCTTAAGTACCTGGCTTGTAAAGAACAGATACTCATGTTAAGGTAGAACGTTAAGCTTCTGGGTATCTGAAACAGGAG	240
81	P L E I G K S L E I R R D I I D L E D D V V A M T S D C D I Y Q T L R G Y A	120
241	CCTTGAAATTCGAAAGAGCTGGAAATAAGAACAGAACAGGACATCATGACTTGGAGGTGATGTTGGCATGGACCGTGTGACATTATAGACTCTAAAGGTTATGCT	360
121	Q K L V S K E E K S F P I A Y S L V V H K D A I M V E R L I H A I Y N Q H N I Y	160
361	CAAAAGCTTGTCTCAARGGGAGAAAAGCTTCCCAATAGGCTATCTTGTGTTGCTCCACAGATGCAATTATGGTTGAAGGCTTATCCATGTTATAACAGCACATATTAC	480
161	C I H Y D R K A P D T F K V A M N N L A K C F S N I F I A S K L E A V E Y A H I	200
481	TGGATCCATTATGATCGTAAGGCACTGTACCTCTAACAGTGGCATGAAACATTAGGTTAACGTCCTCAAAATTTCATTGCTCAAATTAGGGCTGTGMMATATGCCACATT	600
201	S R L Q A D L N C L S D L L K S S I Q W K Y V I N L C G Q D F P L K S N F E L V	240
601	TCGAGACTCAGGCTGATTAAATTGCTTCAGTCAATCCAGTGGAAATAATGTTATCAACTTGTGGCAAAATTGGCTTAACTGTTAAGTCAATTGTTGAATTGGTGTG	720
241	S E L K K L N G A N M L E T V K P P N S K L E R F T Y H H E L R R V P Y E Y V K	280
721	TCAGAGTGAAAAACCTCATGGACCAAAATGTTGGAGACGGTGAACACCCCAAAACAGTAATTGGAAAGATTCACTTACCATGAACTTGTGGCCCTTATGAAATGTTGAAG	840
281	L P I R T N * S K E A P P H N I Q I F V G S A Y F V L S Q A F V K Y I F N N S I	320
841	CTACCAATAAGGAAACATCTCCAGGAACACCCCTAACATCAGATAATTGGCTGGCAGTGTCTTGTAAATAATATTTCACACACTCATC	960
321	V Q D F F A W S K D T Y S P D E H F W A T L I R V P G I P G E I S R S A Q D V S	360
961	GTTCAGAACTTTTGCCTGGTCAAGACATACTCTGTGAGCACTTTGGCTACCTGTGATCGGGTCCAGGAATACTGGGAGATTCAGTCAGGCCAGGTGTGTCT	1080
361	D L Q S K T R L V K W N Y Y E G F F Y P S C T G S H L R S V C I Y G A A E L R W	400
1081	GATCTGAGAGTAACTGACTCGCCTTGTCAAGTGGAAATTACTATAAGGCTTCTATCCAGTTGACTGGATCTACCTCTGAGCTGTGTTATTTGTTAAGGTTGG	1200
401	L I K D G H W F A N K F D S K V D P I L I K C L A E K L E E Q R D W I T L P S	440
1201	CTTATCAAGATGGACATTTGTTGCTAAATAATTGATCTAAGGTGGACCCATCTGATTAAATGCTGGCAGAAAGCTGAGACTGGATCACTTTGCCCCCTCA	1320
441	E K L F M D R N * L T T S *	453
1321	GAAGATTATTATGGATGAAATCTACACACATGAA	1362

C2Gnt3	MKIEKCYFRHIIQKVEILFII-TLWNSLSEKILNVRRIFPQKDIIYVEYLSTSPFVRN-RXTHVKDEVRYEVNCSGYEOPLE	:	83
C2Gnt2	-----MVQWKRICOLHYLWANGCMMATVAIILSFRIKCDSDHGLLESRESOQCRNITXONFLKPKRSINCSGVTRGDEA	:	80
C2Gnt1	-----MLRTEURRRESYPTKYLITESVLRILHOKREYEVSVR-----H-ELAGENPSS-DINCTKVLQGDYNE	:	69
IGnT	-----MPSMRYFELISVSSVIIIFSVENEG-----GDBSSQRLN-----ISDELRITQVCTSFINC-----	:	54

C2Gnt3	IGKS-----LEIRRDIIDDEDVVAMTSDCDIIYQFLRGYAOKLVSKKEKSEPIAYSVLWVKDAIIVVERLTHANOHNTYCHY	:	164
C2Gnt2	VLOAIIENNLEVKREI-FDTHLISLTDCEHKAERKFIGFBTSEEVEFPIAYSMVTHEKTEENERLDRAYAQPNTYCYHAY	:	164
C2Gnt1	NOVKVKEILTVKREKREWPPDDAINTSDCSSEKIKRKYIVEPLSKKEAEFPIAYSVLWVKDAIIVVERLTHANOHNTYCHY	:	154
IGnT	-----K-----TREFLWKNRNMTHERSSCKEYLQOSHYIYTAEPLSKKEAEFPIAYSVLWVKDAIIVVERLTHANOHNTYCHY	:	126

C2Gnt3	DRKABDETEKAMNNLKCCESNIEFASKLEAVEYTHISRELOADINCSDLICKSIIQMKYVINCQGDDEFPLKSNFELVSELKKINGA	:	249
C2Gnt2	DEKSEEEFREAKKAIISCCENVEFASKLVRVWVIAQSWRVAQDINGMEDLQSPWPKYELNTCTGTDDEFPLKSNAEMVQALKMINGR	:	249
C2Gnt1	DIKSEEDSYLAAMGAEASCESNVEFASKLVRVWVIAQSWRVAQDINGKDIYAMSANXKYLINIEGMDDFPKTNLEIVRKKLIMGE	:	239
IGnT	-----DEKATTEERDAVEQLLSCFENAPLASKMEPVWGGISRELOADINCIRDLSAFEVMSKVKVINCQGDDEFPLKTNKEIVQYLGKFGK	:	211

C2Gnt3	NMIEEVKRPNSKLERFTYHLLRPUVYEVKIPFRENTISKEAPPINQEFVGSAVEVYISQAEVKIENNSIVQDEFANSKDTYNSP	:	334
C2Gnt2	NSMEESEVPPKKEETRKYLFEEVNE-----TIL-TINKKDDEPPYNTMETGNAIIVASDENQHVIKNPSSQOLIEWVKDTYNSP	:	328
C2Gnt1	NNNNTTMRMPSSKKEERWKRYEVNE-----RITN-TGTGTVMLPPELTPLESGSAYEVSVREYVGIVINEKICKLMEWAQDTYNSP	:	318
IGnT	-----NITPGVLEPAHAIGRTKVKHQEHLIS-----KELSYVBTITALKPEPENETYFGSAYVALSREEANFVILQWNSKDTYNSP	:	294

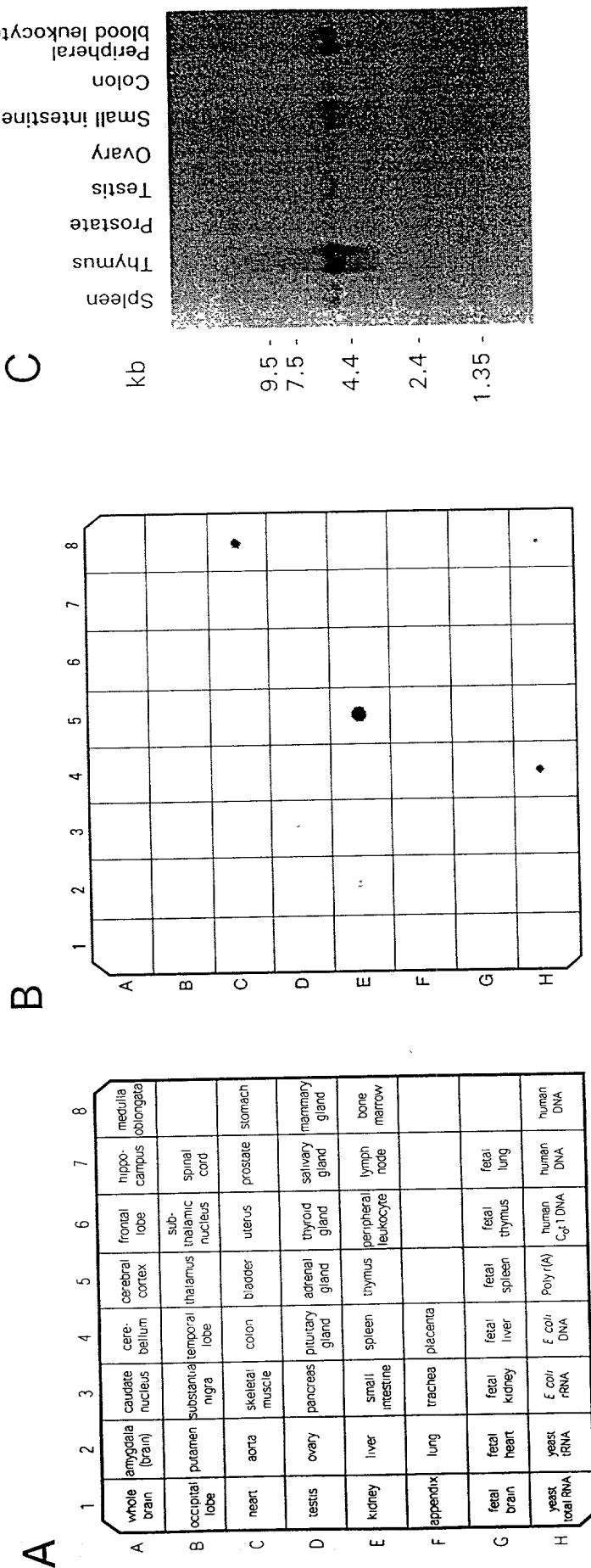
  

C2Gnt3	DEHEWATLIRVPCIPGEITRS-AODVSDLOSSKTREVKNNVYES-----FETESCTGSHLSVCITYGAELIRWLIKDGHEWANKED	:	413
C2Gnt2	DEHEWATLORARWMPGSVPNHP-----DISDNTSIAIREVKWNGOGHEGELDRCGAPYAFCSGIHQRAICVIGADDLNMMTQHLLANKED	:	413
C2Gnt1	DEHEWATLIREPVPGSMPNA-----DEYIWTIONREPVPGSMPNA-----GNIIRAIKWSMED-----RHGGCHGHYVHGGCITYGNGDLKMEVNSPSTEANKEE	:	403
IGnT	-----DEHEWMTINRPEPVPGSMPNA-----SWT-----GNIRAIKWSMED-----RHGGCHGHYVHGGCITYGNGDLKMEVNSPSTEANKEE	:	367

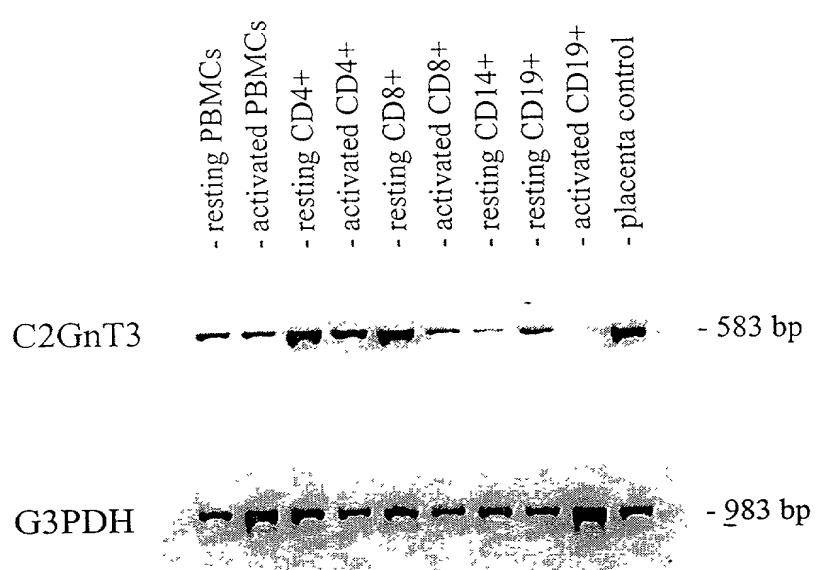
  

C2Gnt3	SKYDPEILIKCIAAEKLEEQQORDWITIPSEKIFMDRNLTTS	:	453
C2Gnt2	-----PDDDNAOCLEEEYLRY-----TIGTE-----	:	438
C2Gnt1	-----VDDLF-----CIDEHLR-----TETLKH-----	:	428
IGnT	-----INTYLTIVECIDEHLRER-----TINQSETAIQPSWYF--	:	400

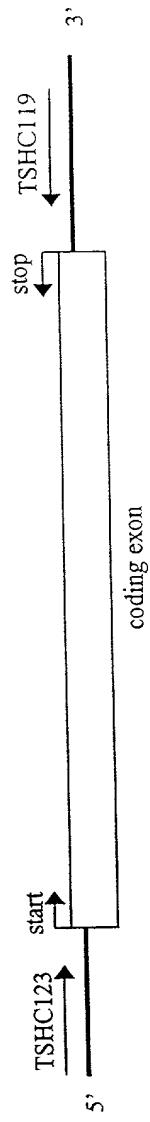
Fig. 3



**Fig. 4**



C2GnT3



TSHC123: 5'-GGGCAGCATTGCCCTAGTATG-3'

TSHC119: 5'-GATCTCTGATTTGGCTCAGTG-3'

Fig. 5